Application No.: 10/724,264

Attorney Docket No.: 02716.0005.NPUS01

THE AMENDMENTS

In the Claims:

(Previously Presented) A proteorhodopsin mutant having improved optical characteristics, said mutant is a proteorhodopsin variant comprising a mutation in a conserved histidine residue. said proteorhodopsin variant having at least 90% identity with its corresponding naturally occurring proteorhodopsin, said conserved histidine is present at the position equivalent to position 75 of SEQ ID NO: 3 when the proteorhodopsin variant is aligned with SEQ ID NO: 3 for maximum identity, wherein said proteorhodopsin mutant has lower pK_{rh} in comparison with the proteorhodopsin variant.

2-3. (Cancelled)

- (Previously Presented) 4. The proteorhodopsin mutant according to Claim 1, wherein said naturally occurring proteorhodopsin comprises SEQ ID NO: 1, 3, 27, 103, 121, 125, 133, 139, 151, or 161.
- 5. (Previously Presented) The proteorhodopsin mutant according to Claim 4, wherein said naturally occurring proteorhodopsin comprises SEQ ID NO: 1 or SEQ ID NO: 3.
- 6. (Cancelled)
- The proteorhodopsin mutant according to Claim 1, wherein said 7. (Previously Presented) conserved histidine residue is mutated to an amino acid capable of forming a hydrogen bond.
- (Original) The proteorhodopsin mutant according to Claim 7, wherein said amino acid 8. capable of forming a H-bond is asparagine, glutamine, lysine, arginine, tryptophan, serine, threonine, tyrosine, aspartic acid, or glutamic acid.
- (Original) The proteorhodopsin mutant according to Claim 8, wherein said amino acid 9.

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capable of forming an H-bond is asparagine, glutamine, lysine, tryptophan, aspartic acid, or glutamic acid.

10-13. (Cancelled)

14. (Previously Presented) The proteorhodopsin mutant according to Claim 1, comprising the amino acid sequence of SEQ ID NO: 165.

15. (Cancelled)

- 16. (Currently Amended) A method for preparing the proteorhodopsin mutant having improved optical characteristics according to Claim 1, comprising the steps of:
 - (a) identifying the conserved histidine amino acid residue of the naturally occurring proteorhodopsin or the proteorhodopsin variant of claim 1,
 - (b) mutagenizing the conserved histidine amino acid residue, and obtaining proteorhodopsin mutants,
 - (c) determining the optical characteristics of the proteorhodopsin mutants, and
 - (d) selecting the proteorhodopsin variant mutant having improved optical characteristics.

17-18. (Cancelled)

19. (Previously Presented) The method according to Claim 16, wherein said conserved amino acid residue is mutagenized by site-directed mutagenesis.

20-22. (Cancelled)

23. (Previously Presented) The proteorhodopsin mutant according to Claim 1, wherein the proteorhodopsin variant has at least 97% identity with the naturally occurring proteorhodopsin.

24. (Cancelled)

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25. (Previously Presented) A proteorhodopsin mutant having improved optical characteristics, said mutant is a proteorhodopsin variant comprising a mutation in a conserved histidine residue, said proteorhodopsin variant is selected from the group consisting of SEQ ID NO: 1, 3, 27, 103, 121, 125, 133, 139, 151, and 161, or having at least 90% identity with the naturally occurring proteorhodopsin, said conserved histidine is present at the position equivalent to position 75 of SEQ ID NO: 3 when the proteorhodopsin variant is aligned with SEQ ID NO: 3 for maximum identity, wherein said proteorhodopsin mutant has lower pK_{rh} in comparison with the proteorhodopsin variant.

- 26. (Previously Presented) The proteorhodopsin mutant according to Claim 25, wherein the proteorhodopsin variant has at least 97% identity with the naturally occurring proteorhodopsin.
- 27. (Previously Presented) The proteorhodopsin mutant according to Claim 25, wherein the naturally occurring proteorhodopsin comprises the amino acid sequence of SEQ ID NO: 3.